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RAW SEQUENCE LISTING
PATENT APPLICATION ***US/08/943,144***

DATE: 05/06/98
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This Raw Listing contains the General Information Section and up to the first 5 pages.

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                              SEQUENCE LISTING

(1)    General Information:

     (i) APPLICANT: KOSHIBA, TOMOKAZU

    (ii) TITLE OF INVENTION: ALDEHYDE OXIDASE GENE DERIVED FROM PLANT
              AND UTILIZATION THEREOF

   (iii) NUMBER OF SEQUENCES: 15

    (iv) CORRESPONDENCE ADDRESS:
          (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
          (B) STREET: P.O. BOX 747
          (C) CITY: FALLS CHURCH
          (D) STATE: VIRGINIA
          (E) COUNTRY: UNITED STATES OF AMERICA
          (F) ZIP: 22040-0747

     (v) COMPUTER READABLE FORM:
          (A) MEDIUM TYPE: Floppy disk
          (B) COMPUTER: IBM PC compatible
          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
          (A) APPLICATION NUMBER: US 08/943,144
          (B) FILING DATE: 03-OCT-1997
          (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
          (A) NAME: STEWART, RAYMOND C.
          (B) REGISTRATION NUMBER: 21,066
          (C) REFERENCE/DOCKET NUMBER: 2185-208P

    (ix) TELECOMMUNICATION INFORMATION:
          (A) TELEPHONE: (703)205-8000
          (B) TELEFAX: (703)205-8050


(2) INFORMATION FOR SEQ ID NO:1:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4412 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: maize (Zea mays L.)
(B) STRAIN: cultivar: Golden Cross Bantam 70

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 46..4119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTGCTGTGTT GTGCTGTGCT GCGTGCTGTG GAGGGGGAGG AGGAG ATG GGG AAG          54
                                                  Met Gly Lys
                                                    1

GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC AAC GGC        102
Glu Ala Gly Ala Ala Glu Ser Ser Thr Val Val Leu Ala Val Asn Gly
  5                  10                  15

AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG CTG GAG        150
Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser Leu Leu Glu
 20                  25                  30                  35

TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC TGC GGC        198
Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly
                 40                  45                  50

GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC GAC CCG        246
Glu Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro
             55                  60                  65

GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG ACG CTG        294
Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu
         70                  75                  80

CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA ATC GGC        342
Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly
  85                  90                  95

AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC GGC TTC        390
Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe
100                 105                 110                 115

CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG TCC ATC        438
His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile
                120                 125                 130
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100  TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG GAC CCT      486
101  Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg Pro Asp Pro
102              135                 140                 145
103
104  CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG GCT GTC      534
105  Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu Lys Ala Val
106          150                 155                 160
107
108  TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT GAC ACC      582
109  Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Thr
110      165                 170                 175
111
112  TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC CTC AAC      630
113  Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu Gly Leu Asn
114  180                 185                 190                 195
115
116  TGT TTC TGG AAG AAG GGC GAA GAA CCT GCA GAA GTC AGC AGG CTG CCG      678
117  Cys Phe Trp Lys Lys Gly Glu Glu Pro Ala Glu Val Ser Arg Leu Pro
118                  200                 205                 210
119
120  GGG TAC AAC AGC GGT GCC GTC TGC ACC TTT CCA GAG TTT CTC AAA TCC      726
121  Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe Leu Lys Ser
122              215                 220                 225
123
124  GAA ATC AAG TCT ACT ATG AAG CAG GTG AAC GAT GTC CCC ATT GCA GCC      774
125  Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro Ile Ala Ala
126          230                 235                 240
127
128  TCA GGT GAT GGC TGG TAC CAT CCT AAG AGC ATT GAA GAG CTT CAC AGG      822
129  Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu Leu His Arg
130      245                 250                 255
131
132  TTG TTT GAT TCC AGC TGG TTT GAT GAC AGT TCT GTG AAG ATT GTT GCT      870
133  Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys Ile Val Ala
134  260                 265                 270                 275
135
136  TCA AAC ACT GGG TCT GGA GTG TAC AAG GAT CAG GAC CTC TAC GAC AAG      918
137  Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys
138                  280                 285                 290
139
140  TAC ATT GAC ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAT AAA AAC      966
141  Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Lys Asn
142              295                 300                 305
143
144  GAC AAA GCA ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA GCT ATT     1014
145  Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile
146          310                 315                 320
147
148  GAA GTG CTG TCA GAT GGA AAT TTG GTC TTC AGA AAG ATT GCT GAT CAC     1062
149  Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Asp His
150      325                 330                 335
151
152  CTC AAC AAA GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC ATA GGA     1110
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153  Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly
154  340                 345                 350                 355
155
156  GGA AAC ATA ATG ATG GCA CAA AGG TTG CCA TTT GAA TCG GAT GTT GCA      1158
157  Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser Asp Val Ala
158                  360                 365                 370
159
160  ACC GTG CTC CTA GCT GCG GGT TCG ACA GTC ACA GTC CAG GTG GCT TCC      1206
161  Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln Val Ala Ser
162              375                 380                 385
163
164  AAA AGG CTG TGC TTC ACT CTG GAG GAA TTC TTG GAA CAA CCT CCA TGT      1254
165  Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln Pro Pro Cys
166          390                 395                 400
167
168  GAT TCT AGG ACC CTG CTG CTG AGC ATA TTT ATC CCA GAA TGG GGT TCA      1302
169  Asp Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu Trp Gly Ser
170      405                 410                 415
171
172  GAC TAT GTC ACC TTT GAG ACT TTC CGA GCC GCC CCA CGA CCA TTT GGA      1350
173  Asp Tyr Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg Pro Phe Gly
174  420                 425                 430                 435
175
176  AAT GCT GTC TCT TAT GTA AAC TCT GCT TTC TTG GCA AGG ACA TCA GGC      1398
177  Asn Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg Thr Ser Gly
178                  440                 445                 450
179
180  AGC CTT CTA ATT GAG GAT ATA TGC TTG GCA TTT GGT GCC TAC GGA GTC      1446
181  Ser Leu Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly Ala Tyr Gly Val
182              455                 460                 465
183
184  GAT CAT GCC ATC AGA GCT AAG AAG GTT GAA GAT TTC TTG AAG GGA AAA      1494
185  Asp His Ala Ile Arg Ala Lys Lys Val Glu Asp Phe Leu Lys Gly Lys
186          470                 475                 480
187
188  TCG CTG AGC TCA TTT GTG ATA CTT GAA GCA ATT AAA CTA CTC AAA GAT      1542
189  Ser Leu Ser Ser Phe Val Ile Leu Glu Ala Ile Lys Leu Leu Lys Asp
190      485                 490                 495
191
192  ACC GTT TCA CCA TCA GAA GGC ACT ACA CAT CAT GAA TAC AGG GTC AGC      1590
193  Thr Val Ser Pro Ser Glu Gly Thr Thr His His Glu Tyr Arg Val Ser
194  500                 505                 510                 515
195
196  TTG GCT GTC AGT TTC TTG TTC AGT TTC TTA TCT TCC CTT GCC AAC AGT      1638
197  Leu Ala Val Ser Phe Leu Phe Ser Phe Leu Ser Ser Leu Ala Asn Ser
198                  520                 525                 530
199
200  TCG AGT GCA CCA TCA AAT ATT GAT ACT CCC AAT GGG TCA TAT ACT CAT      1686
201  Ser Ser Ala Pro Ser Asn Ile Asp Thr Pro Asn Gly Ser Tyr Thr His
202              535                 540                 545
203
204  GAA ACT GGT AGC AAT GTG GAC TCA CCT GAG AGG CAT ATT AAG GTT GAC      1734
205  Glu Thr Gly Ser Asn Val Asp Ser Pro Glu Arg His Ile Lys Val Asp
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206          550                 555                 560
207
208  AGC AAT GAT TTG CCA ATT CGT TCA AGA CAA GAA ATG GTT TTC AGC GAT      1782
209  Ser Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Met Val Phe Ser Asp
210      565                 570                 575
211
212  GAG TAC AAG CCT GTT GGC AAG CCG ATC AAG AAA GTC GGG GCA GAG ATC      1830
213  Glu Tyr Lys Pro Val Gly Lys Pro Ile Lys Lys Val Gly Ala Glu Ile
214  580                 585                 590                 595
215
216  CAA GCA TCA GGG GAG GCT GTG TAC GTT GAT GAT ATC CCT GCT CCC AAG      1878
217  Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro Ala Pro Lys
218                  600                 605                 610
219
220  GAT TGC CTC TAT GGA GCA TTT ATC TAC AGC ACA CAT CCT CAT GCT CAT      1926
221  Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro His Ala His
222              615                 620                 625
223
224  GTG AGA AGT ATC AAC TTC AAA TCA TCC TTG GCT TCA CAG AAG GTC ATC      1974
225  Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln Lys Val Ile
226          630                 635                 640
227
228  ACA GTT ATA ACC GCA AAG GAT ATT CCA AGC GGT GGA GAA AAT ATT GGA      2022
229  Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu Asn Ile Gly
230      645                 650                 655
231
232  AGC AGC TTC CTG ATG CAA GGA GAA GCA CTA TTT GCA GAT CCA ATC GCT      2070
233  Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp Pro Ile Ala
234  660                 665                 670                 675
235
236  GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT GAA ACA CAA AGA      2118
237  Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu Thr Gln Arg
238                  680                 685                 690
239
240  TAT GCT AAT ATG GCT GCA AAG CAA GCT GTT GTT GAG TAT AGC ACA GAA      2166
241  Tyr Ala Asn Met Ala Ala Lys Gln Ala Val Val Glu Tyr Ser Thr Glu
242              695                 700                 705
243
244  AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCC ATC CAA AGA AAC      2214
245  Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile Gln Arg Asn
246          710                 715                 720
247
248  AGC TAC ATC CAA ATT CCC CCA TTT TTA GCT CCA AAG CCA GTT GGT GAC      2262
249  Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro Val Gly Asp
250      725                 730                 735
251
252  TAC AAC AAA GGG ATG GCT GAA GCA GAC CAC AAG ATT CTA TCA GCA GAG      2310
253  Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu Ser Ala Glu
254  740                 745                 750                 755
255
256  GTA AAA CTT GAA TCC CAG TAC TAC TTC TAC ATG GAA ACT CAA GCA GCA      2358
257  Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr Gln Ala Ala
258                  760                 765                 770
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PATENT APPLICATION *US/08/943,144*

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